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Belize Barrier Reef Transect: How Far Do Coral Reef Fish Larvae Travel In Marine Currents?

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Abstract

The vast majority of coral reef fishes go through a pelagic larval stage, which provides potential for long-distance dispersal by marine currents. Yet planktonic larvae are notoriously difficult to track owing to their small size, and as a consequence the spatial scale of dispersal in coral reef fishes is largely unknown. Robust estimates of dispersal are needed owing to the fundamental importance of this parameter for the design and management of networks of marine protected areas. If larvae disperse locally, geographically nearer individuals are anticipated to be more similar genetically. A pattern of increasing genetic differentiation with geographic distance, referred to as genetic 'isolation by distance', is expected in this case and provides an opportunity to estimate dispersal. A specific aspect of this approach is that it requires the continuous sampling of individuals along a continuous population. The 250 km long Belize Barrier Reef provides an unparalleled opportunity to sample continuously along continuous populations of coral reef fishes. Individuals were collected continuously along a 250-km transect following the Belize Barrier Reef to estimate larval dispersal in seven species of coral reef fish with different life histories.

Keywords: isolation by distance, larval dispersal, microsatellites, population genetics

Introduction

Caribbean coral reefs are declining on a regional scale (Gardner et al., 2003), and associated coral reef fishes are following this trend (Paddack et al., 2009). This ongoing decline calls for the protection of coral reefs and associated fishes, and networks of marine protected areas (MPAs) have emerged as a key conservation and management tool. But how large should be a MPA to be self-sustainable? How far away should different MPAs be located in order to stay demographically connected? To what extent do MPAs contribute to replenish neighboring, non-protected areas? The answers to these questions depend on the spatial scale of dispersal of the organisms living within the MPAs.

In coral reef fishes, the greatest potential for dispersal is provided by the larvae, which can drift in marine currents for days, weeks or months depending on the species. Yet planktonic larvae are notoriously difficult to track owing to their small size, and as a consequence larval movement has been unanimously recognized as a major 'science gap' for the conservation and management of coral reefs (Sale et al., 2005; Cowen et al., 2007; Botsford et al., 2009).

Population genetics provide an appropriate framework to address questions of larval movement. Rousset (2000) showed how the decrease in genetic relatedness between individuals with increasing geographic distance (genetic 'isolation by distance') can be used to estimate dispersal if population density is known. This approach has provided dispersal estimates that are consistent with mark-

recapture estimates of dispersal within a factor of two in reptiles, mammals and insects (Rousset, 2000; Sumner et al., 2001; Broquet et al., 2006; Watts et al., 2007), challenging the notion that genetic and demographic estimates of dispersal are inconsistent. A very specific aspect of this approach is that requires the continuous sampling of individuals along a continuous population.

Methods

A total of 100 regularly spaced sampling sites were considered along a 250 km transect following the Belize Barrier Reef. The indigo hamlet (*Hypoplectrus indigo*), black hamlet (*H. nigricans*), barred hamlet (*H. puella*), bicolor damselfish (*Stegastes partitus*), bluehead wrasse (*Thalassoma bifasciatum*), foureye butterflyfish (*Chaetodon capistratus*) and French grunt (*Haemulon flavolineatum*) were selected as target species because they comprise planktonic larval durations ranging from a few to >45 days typical of most coral reef fishes, because ten or more hypervariable (microsatellite) DNA markers have been developed for all of them, and because they are relatively small and abundant in Belize, facilitating population monitoring and sampling. The objective was to collect one individual of each target species at each sampling site, and perform a 400 m^2 scuba survey every other sampling site to estimate population densities of all target species.

Fieldwork was undertaken between June 26th and July 16th 2010 from the *S/V Legacy*, a 64' 10" liveaboard, crewed custom catamaran specially accommodated for scientists with a 8.5 cfm Bauer compressor and a covered working area. All the fieldwork was realized by a team of five scuba divers including the four authors and Myriam Morneau.

Results

Owing to the early first tropical storm of the season (Alex), we were not able to work at the first 14 sites of the transect. Fieldwork was therefore realized at 86 sites along 210 km of reef, from Ambergris Cay (17º 51.88' N, 87º 58.20' W) to the Sapodilla Cays (16º 4.75' N, 88º 17.00' W). A total of 508 samples were collected, including 52 barred hamlets, 55 indigo hamlets, 66 black hamlets, 82 bluehead wrasses, 85 bicolor damselfish, 83 foureye butterflyfishes and 85 French grunts. Forty-three transects covering a total of 17,200 m^2 of reef were performed. All in all, fieldwork involved more than 300 scuba dives by the five participants. Genetic analyses of all samples have been performed at the Smithsonian Tropical Research Institute in Panama. Preliminary results suggest restricted dispersal (30 km or less) in some, but not all species considered.

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